

Figure 1A.

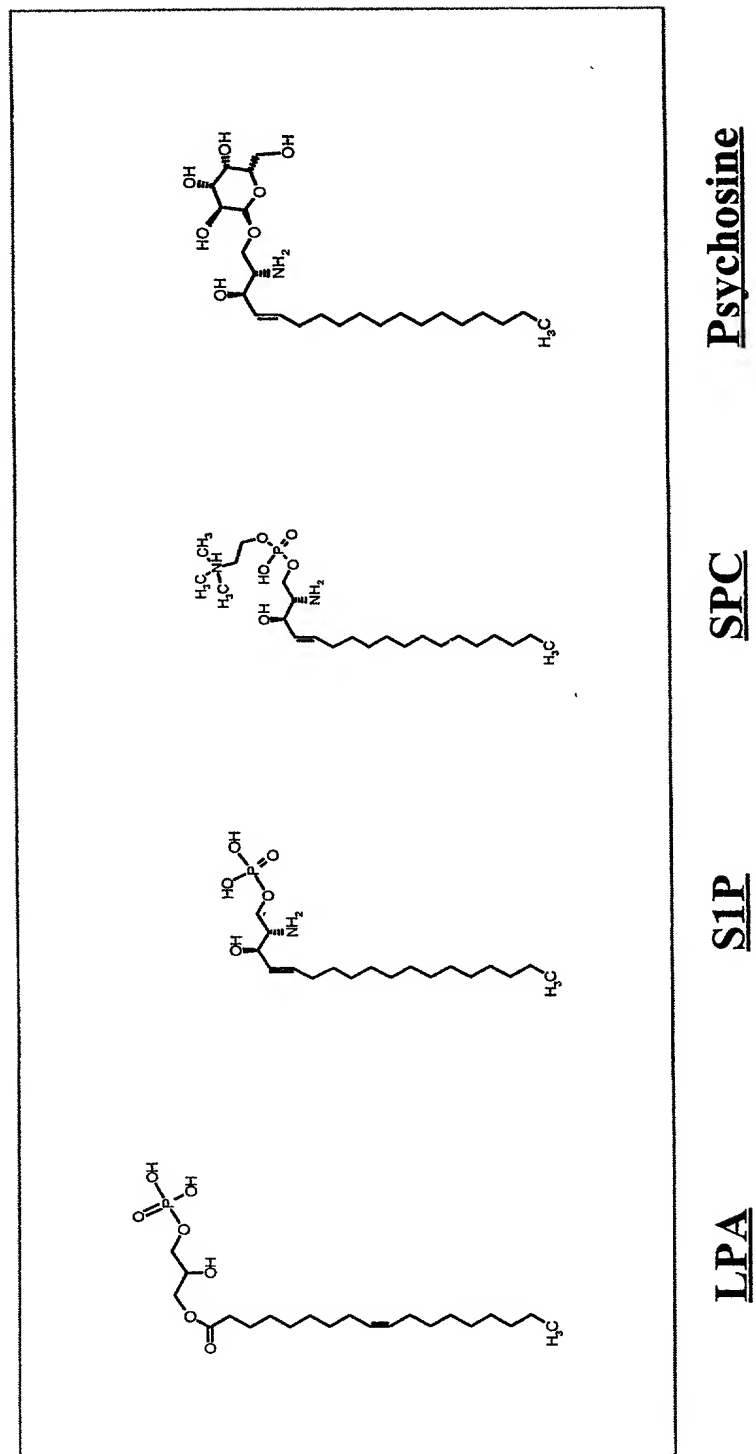


Figure 1B.

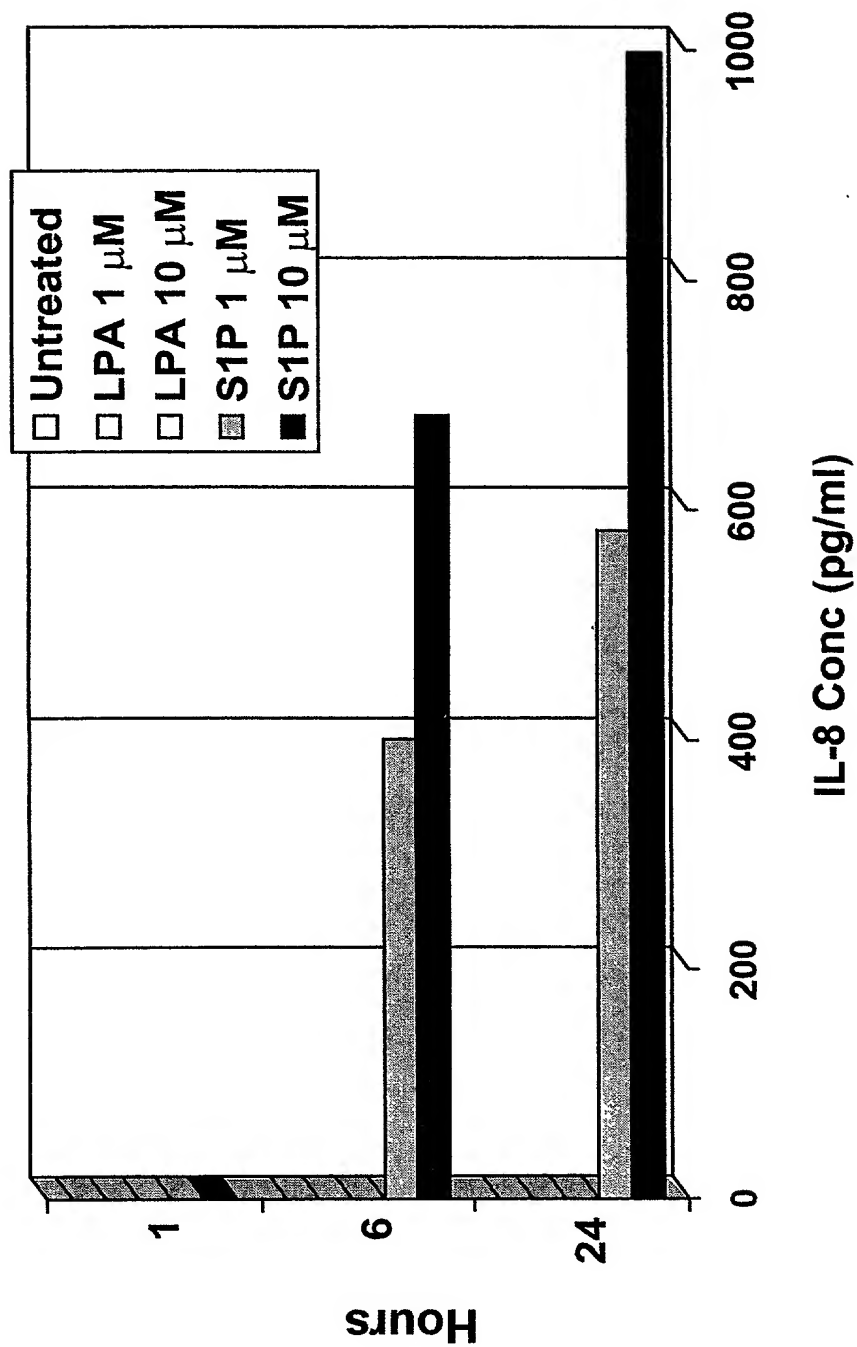


Figure 2A.

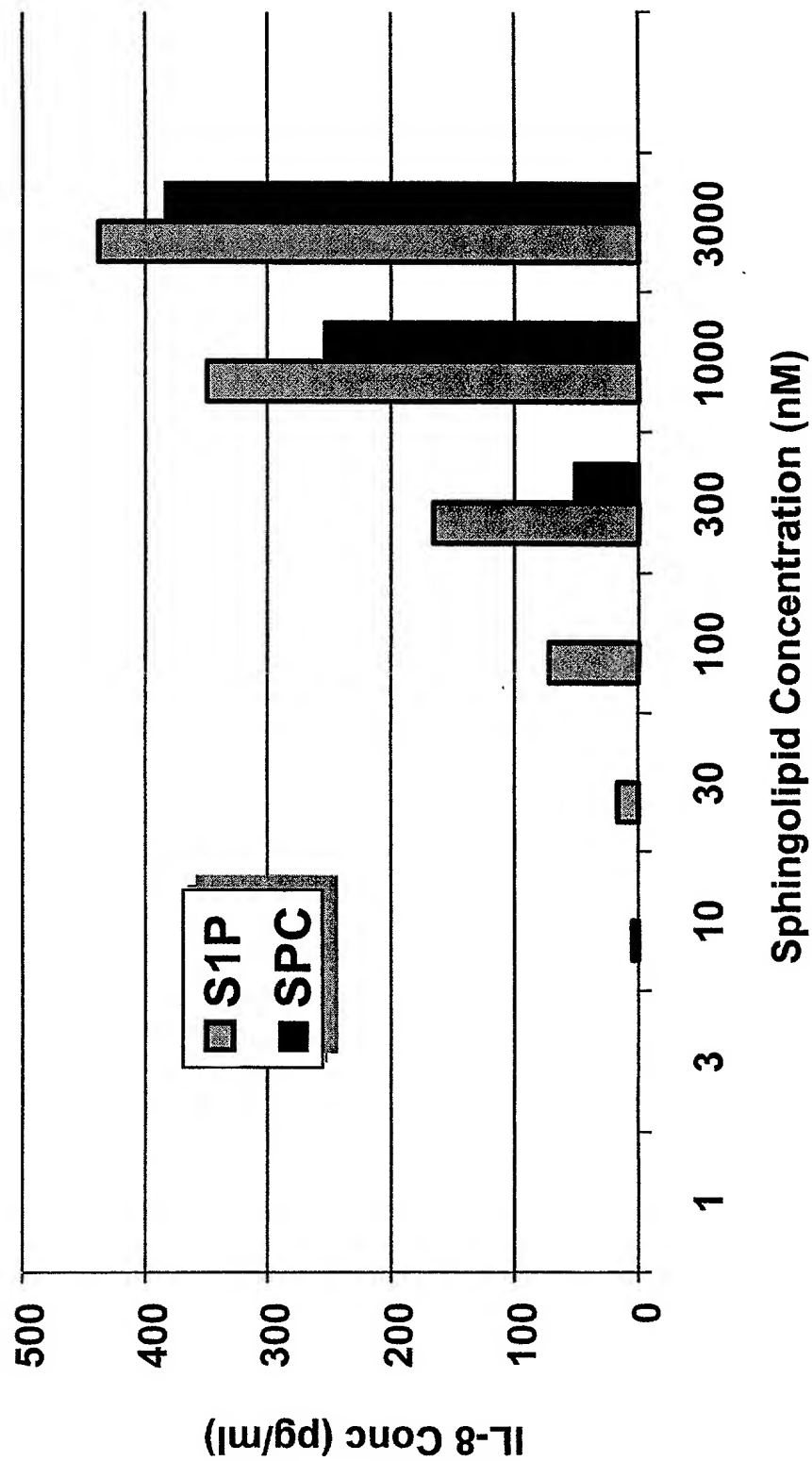


FIGURE 2

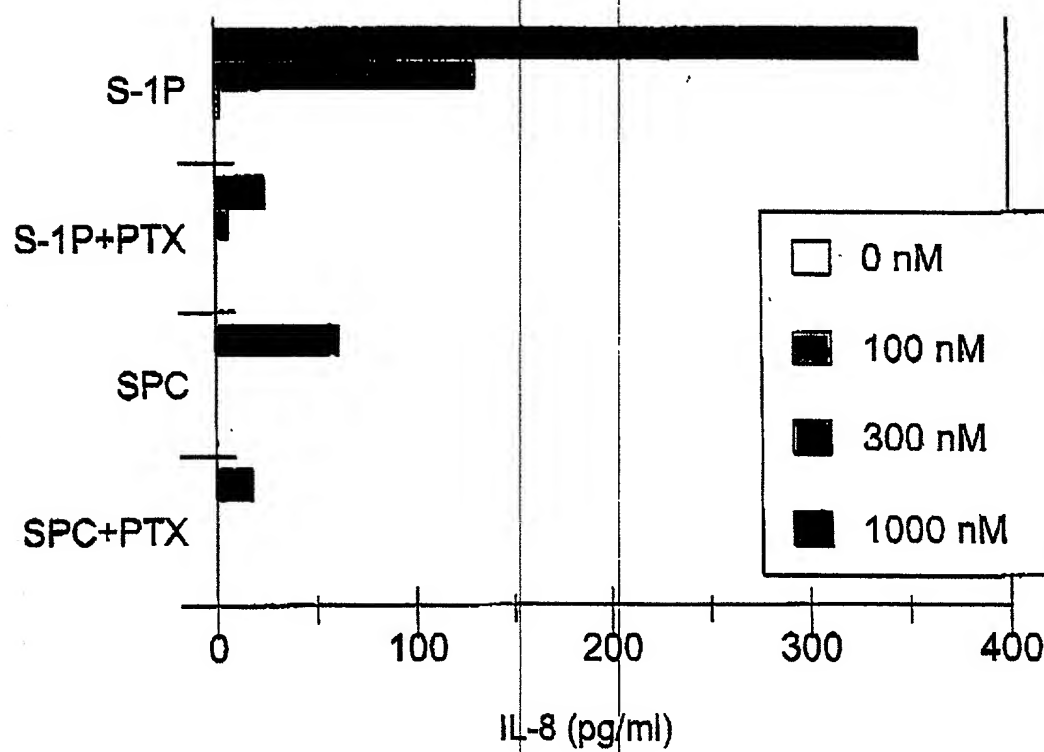


Figure 3.

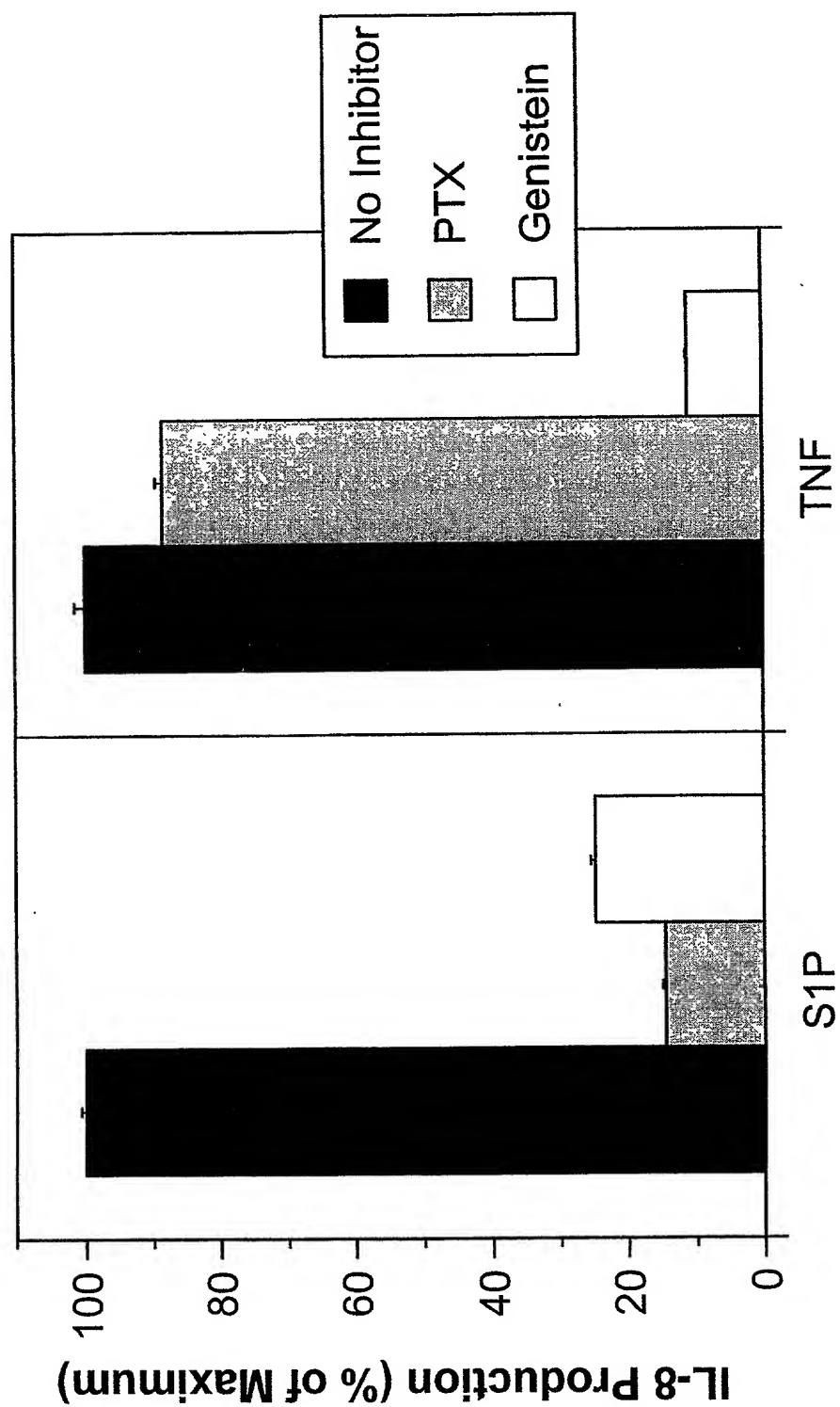


FIGURE 4A

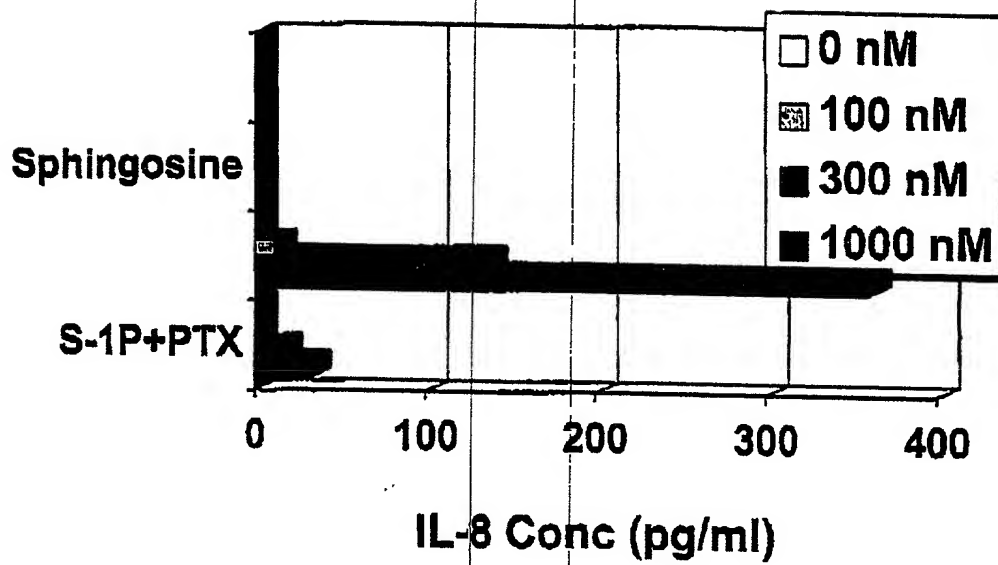


Figure 4B.

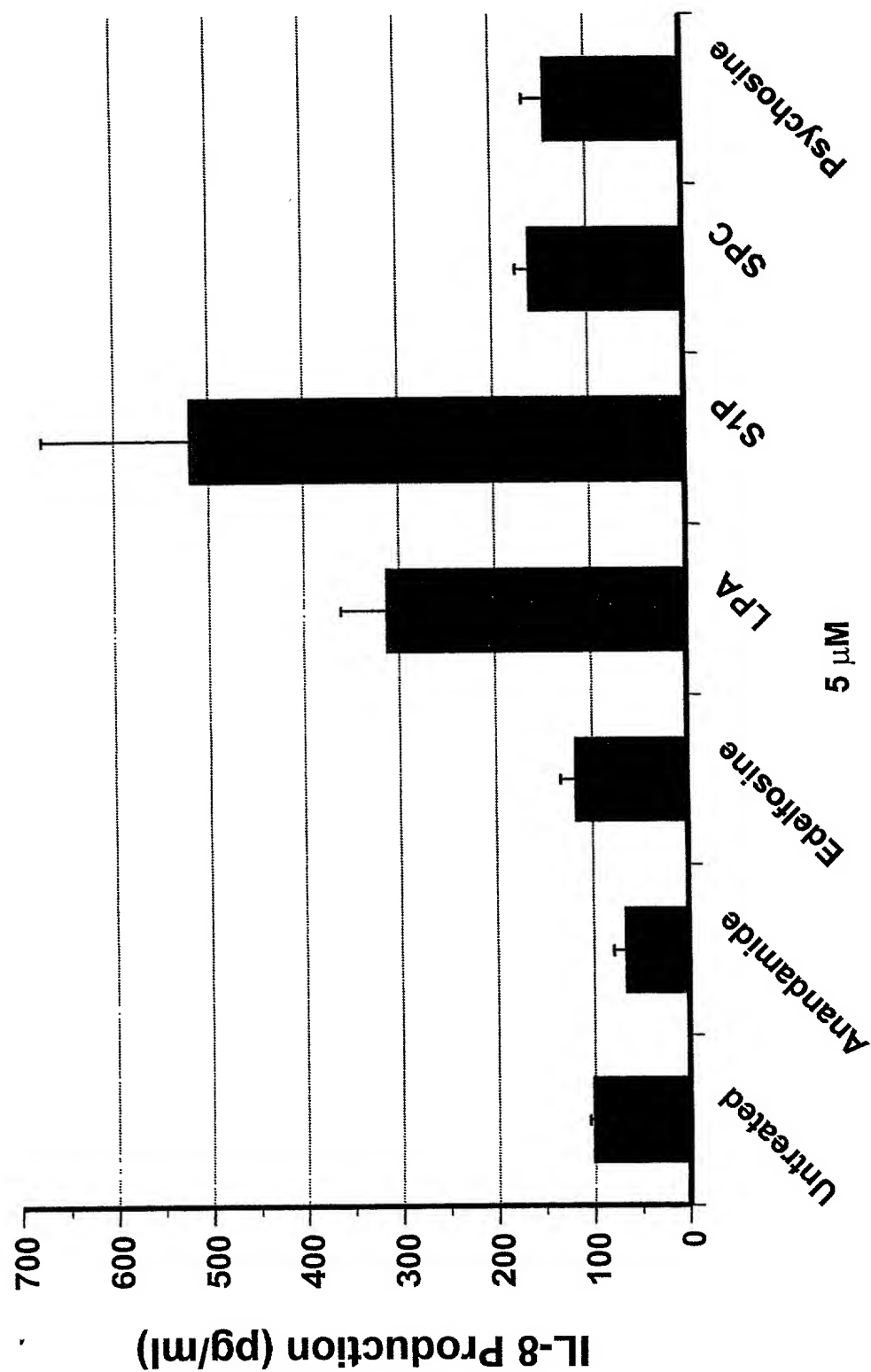


Figure 5.

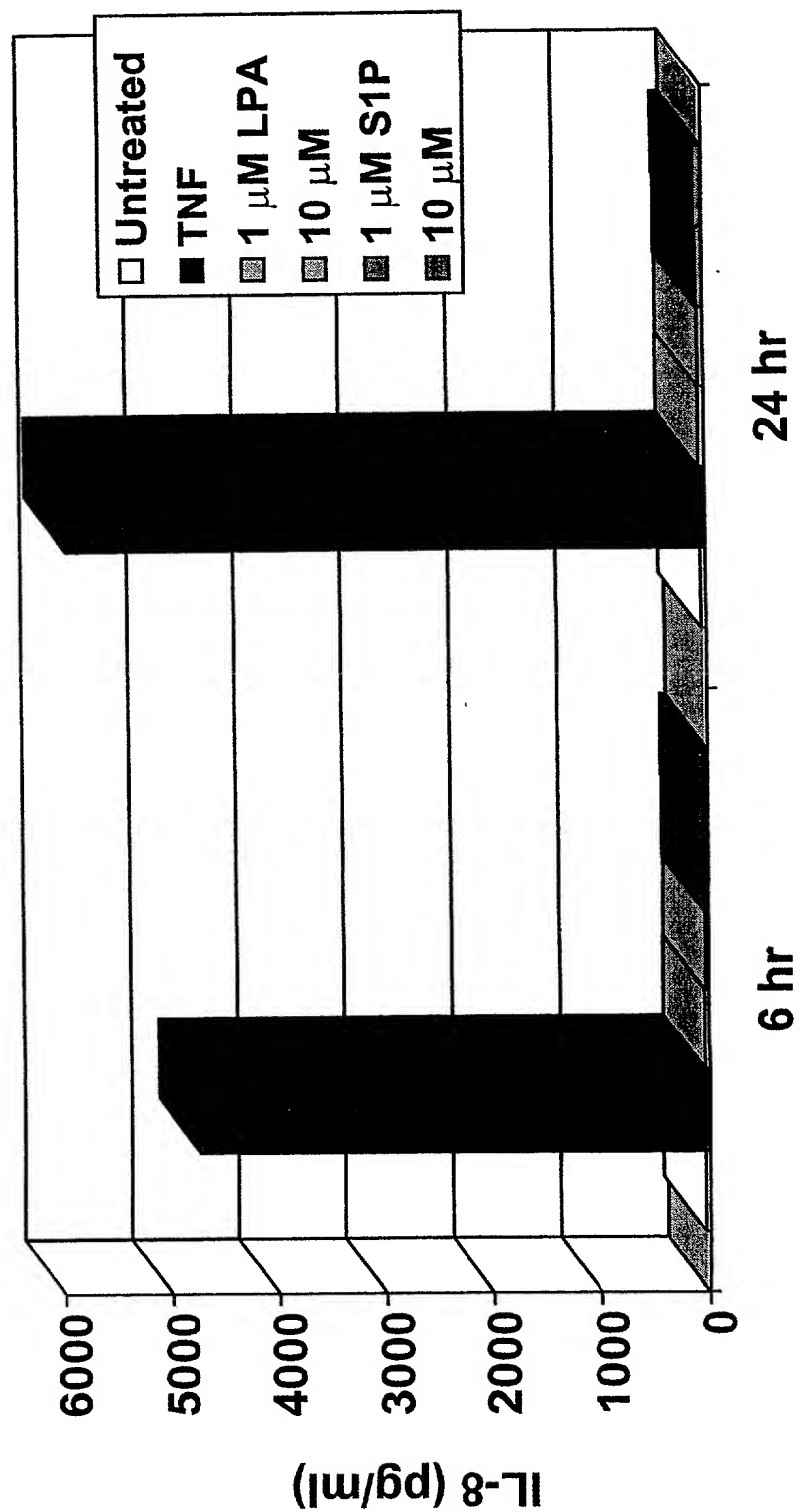
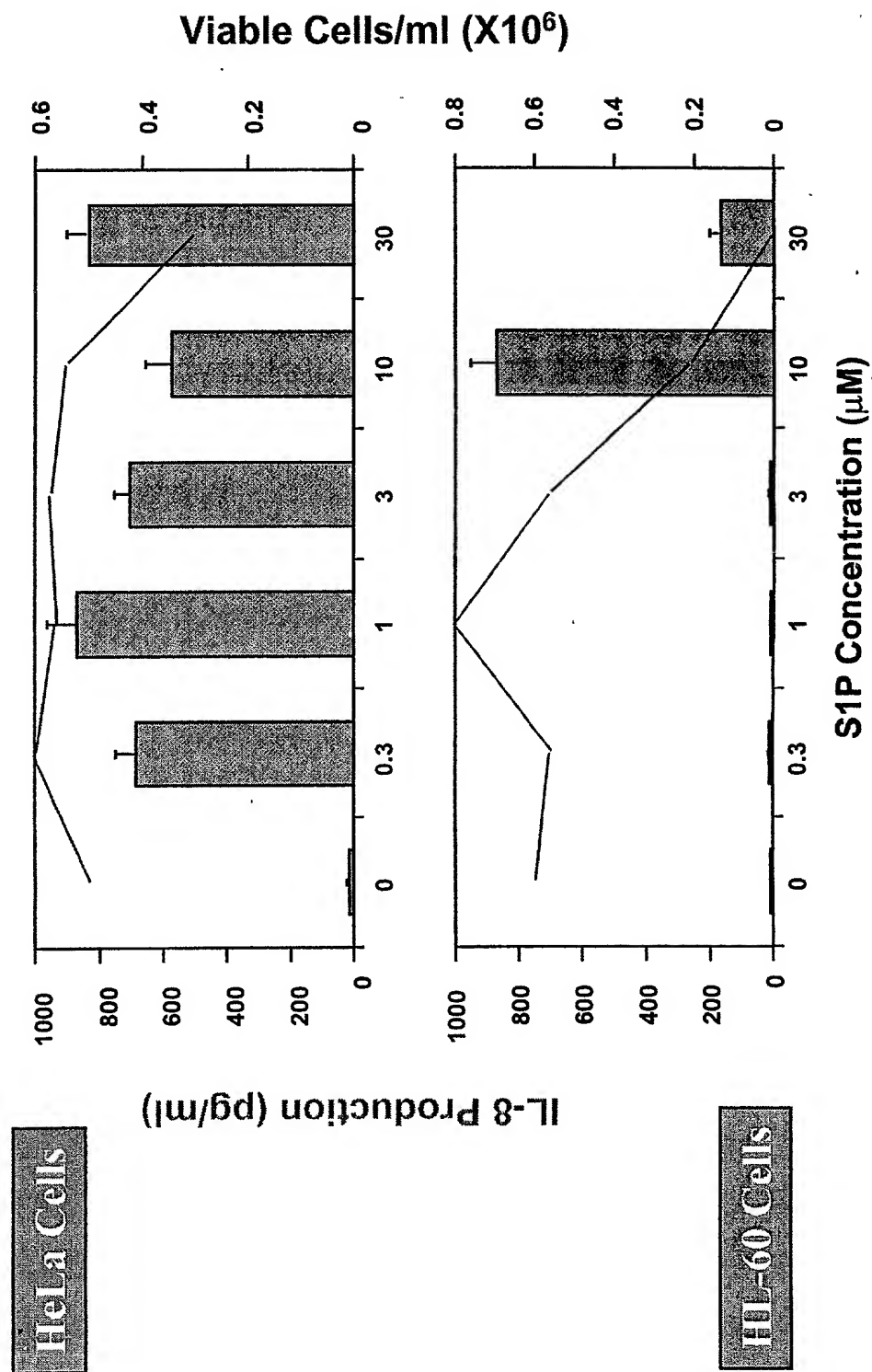


Figure 6.



IL-8 (pg/ml)

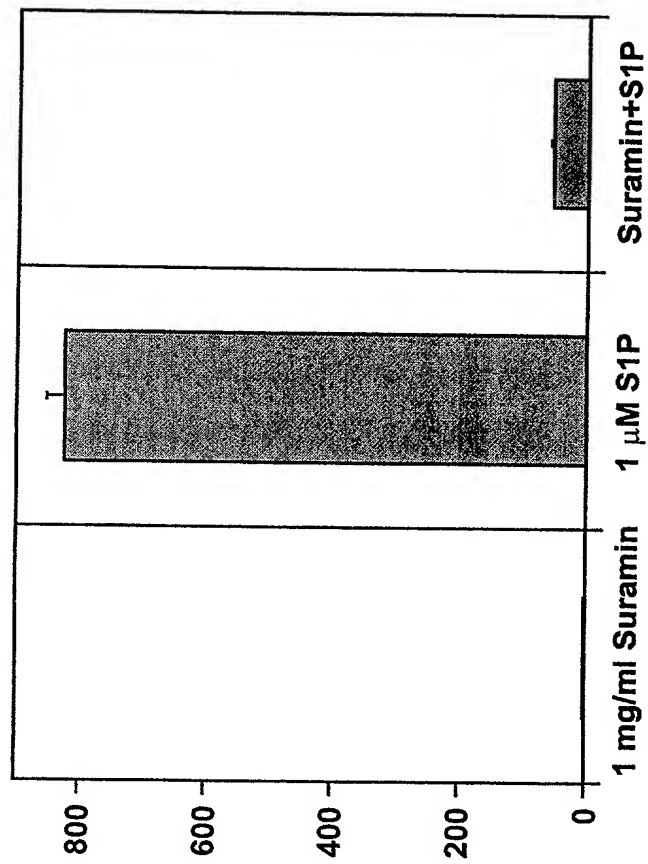


Figure 7.

Figure 8.

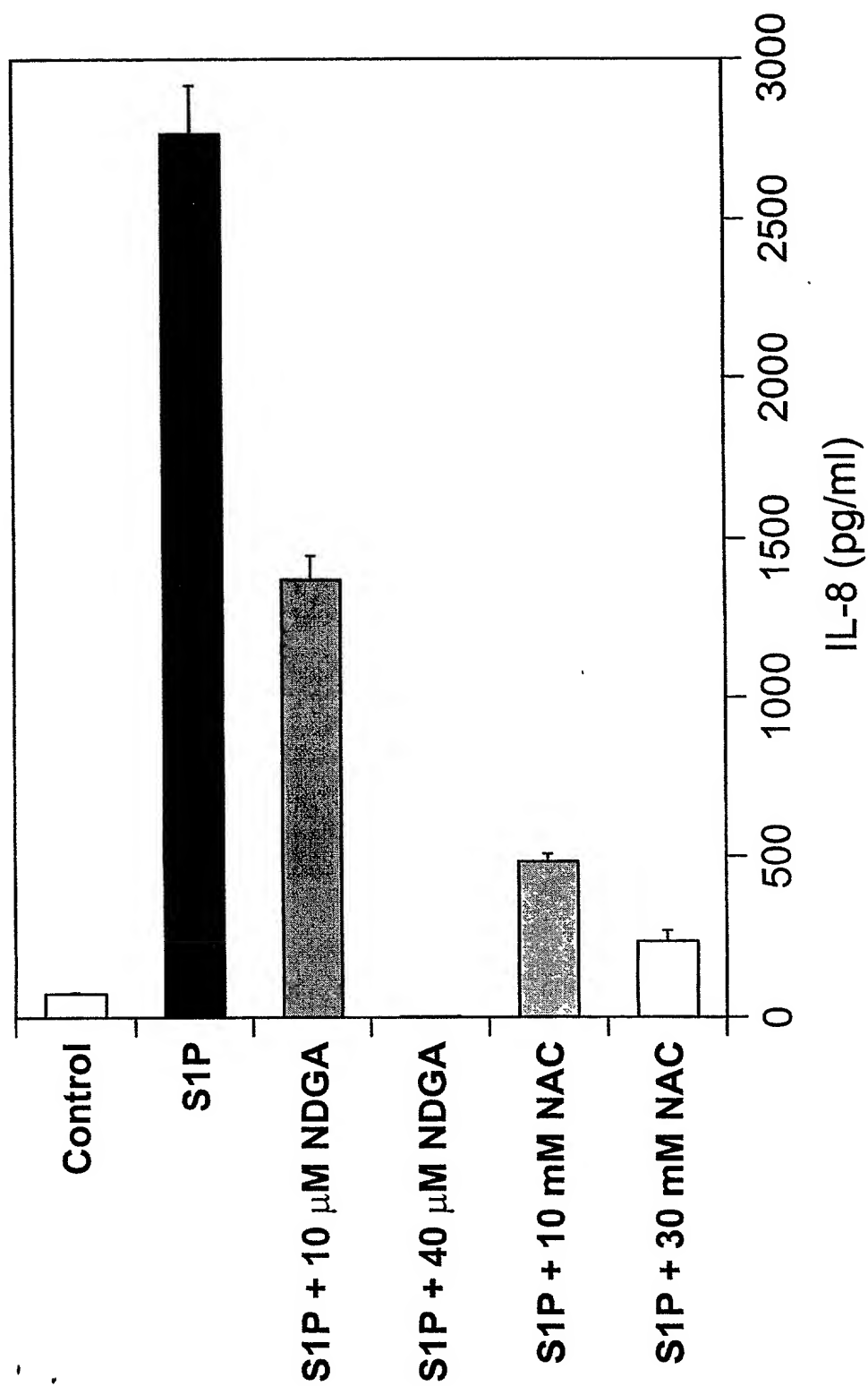


Figure 9.

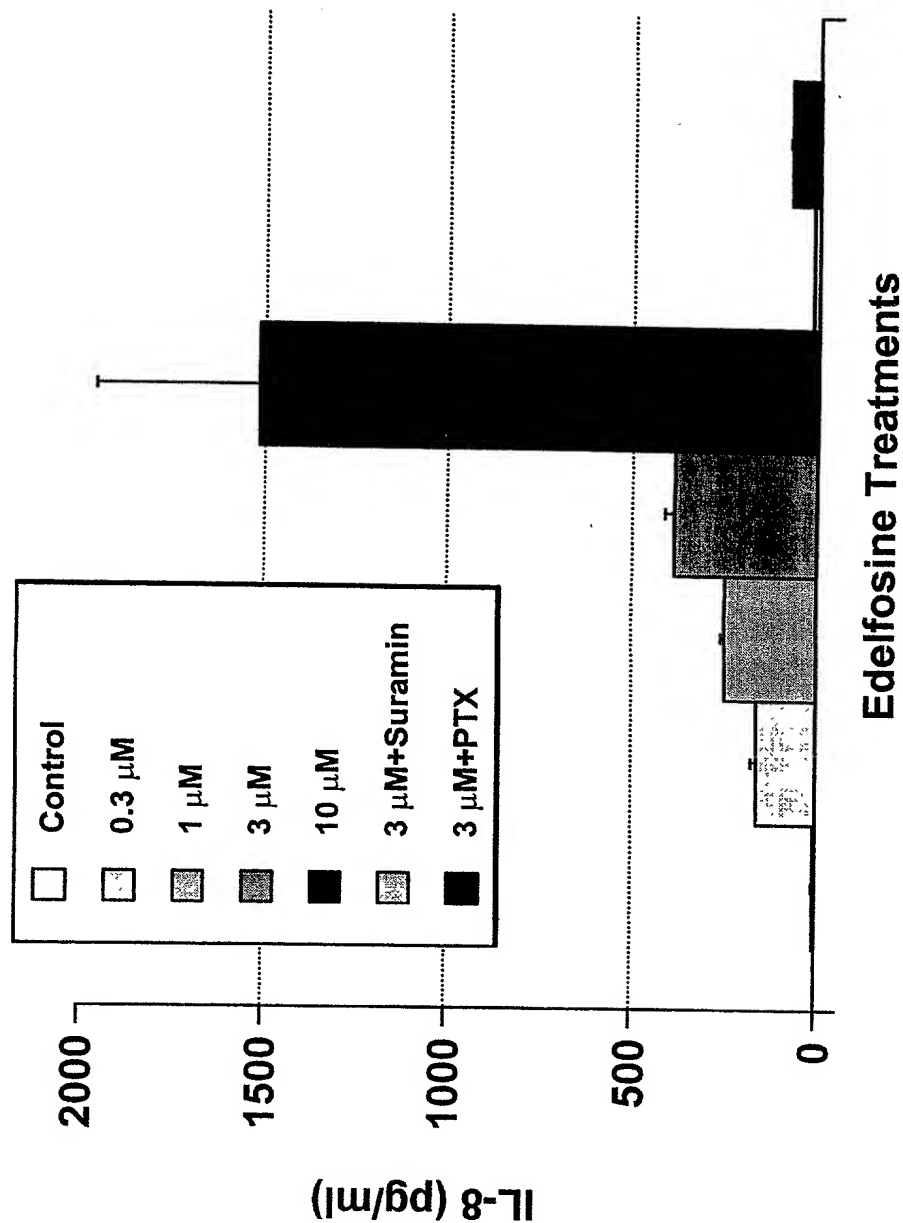


FIGURE 10A

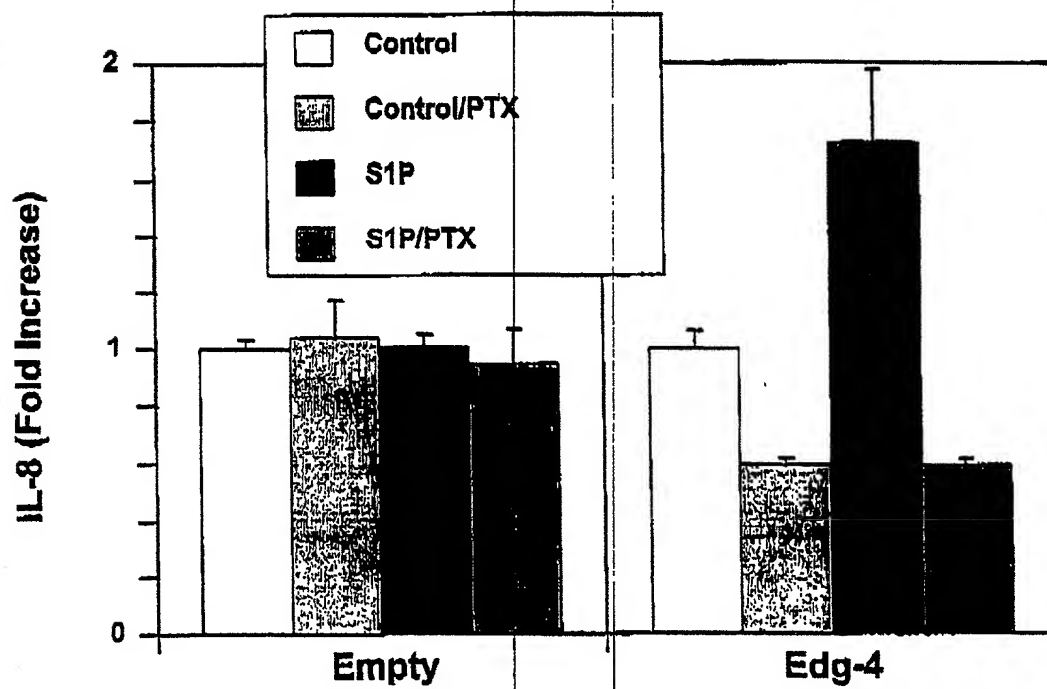


Figure 11.

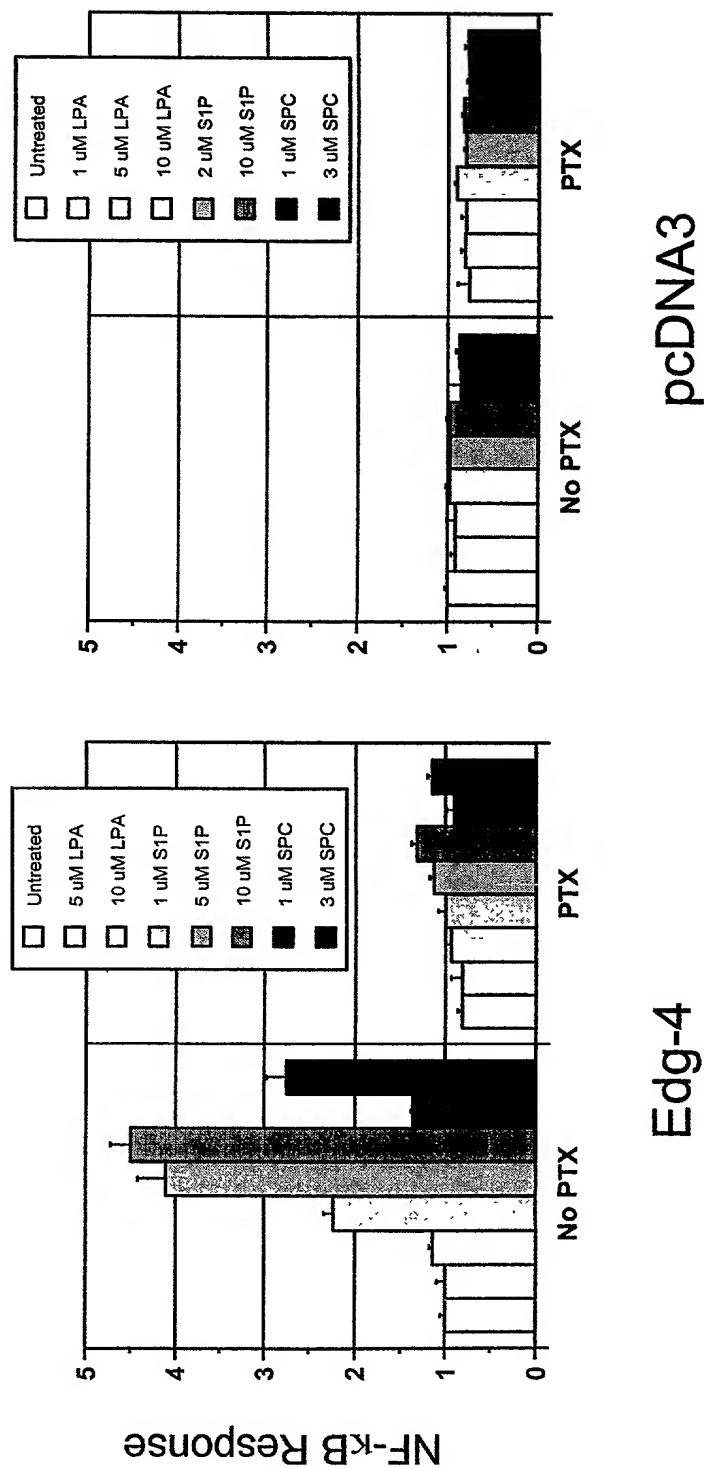


Figure 12.

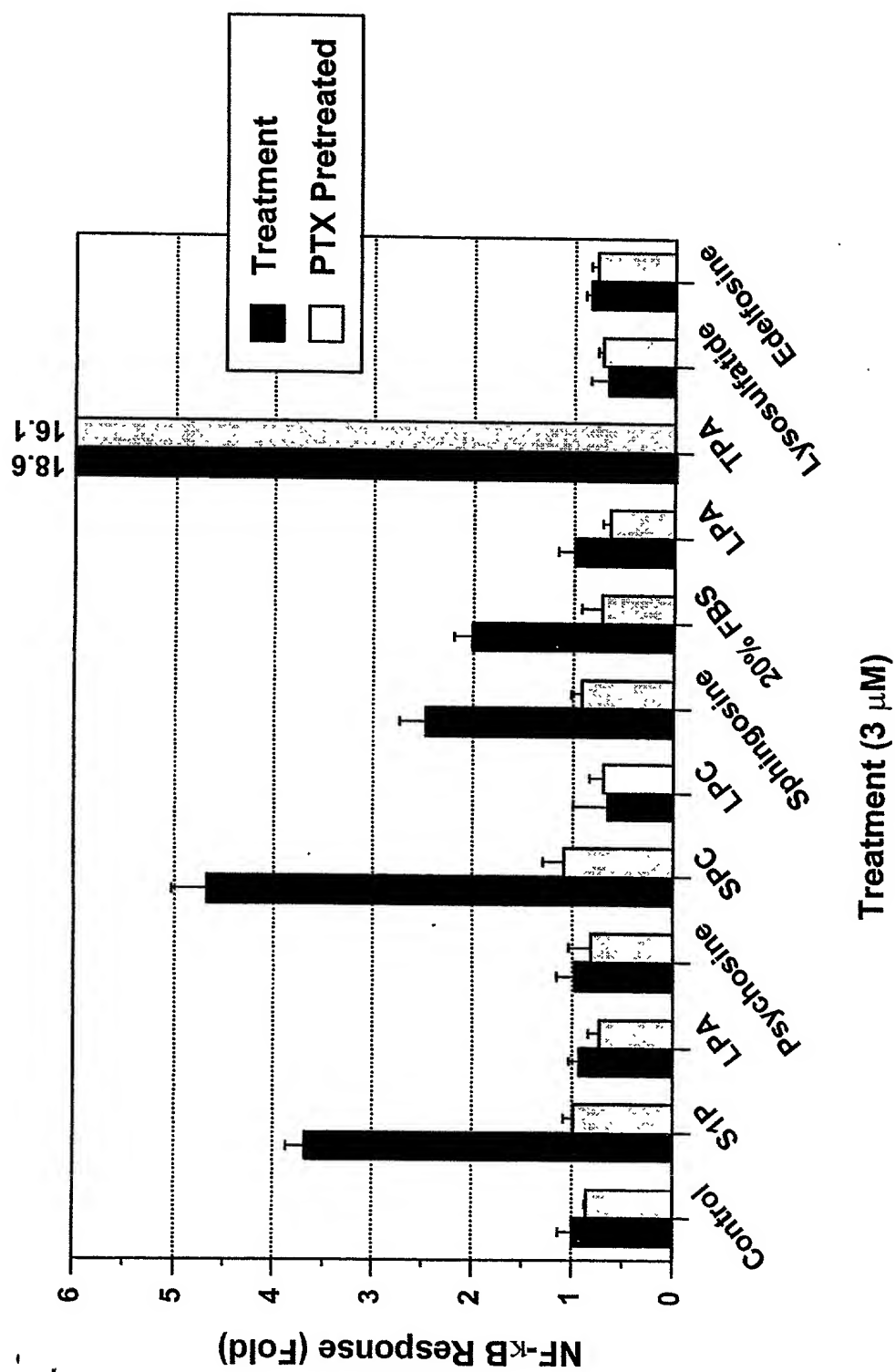


Figure 13.

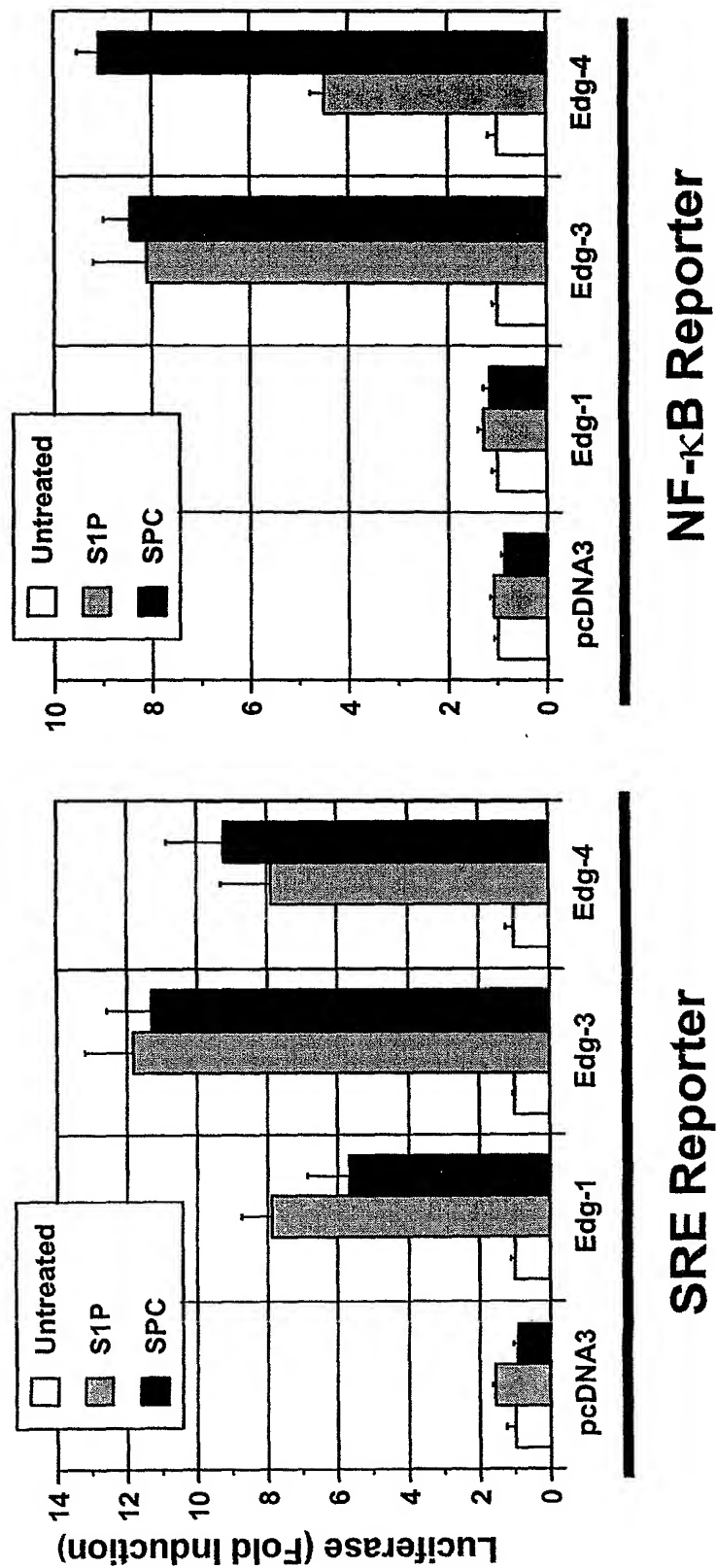


FIGURE 14

| | | | | |
|----------|------------|------------|------------|----------------------------------|
| 1 | | | | 50 |
| AA834537 | -----AAA | GCCCCATGGC | CCCAGCAGGC | CTCTGAGCCC CACCATGGGC |
| AA804628 | -----AAA | GCCCCATGGC | CCCAGCAGGC | CTCTGAGCCC CACCATGGGC |
| AA827835 | AGTTCTGAAA | GCCCCATGGC | CCCAGCAGGC | CTCTGAGCCC CACCATGGGC |
| | 51 | | | 100 |
| AA834537 | AGCTTGTA | CT | CGGAGTACCT | GAACCCCAAC AAGGTCCAGG AACACTATAA |
| AA804628 | AGCTTGTA | CT | CGGAGTACCT | GAACCCCAAC AAGGTCCAGG AACACTATAA |
| AA827835 | AGCTTGTA | CT | CGGAGTACCT | GAACCCCAAC AAGGTCCAGG AACACTATAA |
| | 101 | | | 150 |
| AA834537 | TTATACCAAG | GAGACGCTGG | AAACGCAGGA | GACGACCTCC CGCCAGGTGG |
| AA804628 | TTATACCAAG | GAGACGCTGG | AAACGCAGGA | GACGACCTCC CGCCAGGTGG |
| AA827835 | TTATACCAAG | GAGACGCTGG | AAACGCAGGA | GACGACCTCC CGCCAGGTGG |
| | 151 | | | 200 |
| AA834537 | CCTCGGCATT | CATCGTCATC | CTCTGTTGCG | CCATTGTGGT GGAAAACCTT |
| AA804628 | CCTCGGCATT | CATCGTCATC | CTCTGTTGCG | CCATTGTGGT GGAAAACCTT |
| AA827835 | GCTCGGCCTT | CATCGTCATC | CTCTGTTGCG | CCATTGTGGT GGAAAACCTT |
| | 201 | | | 250 |
| AA834537 | CTGGTGCTCA | TTGCGGTGGC | CCGAAACAGC | AAGTTCACCT CGGCAATGTA |
| AA804628 | CTGGTGCTCA | TTGCGGTGGC | CCGAAACAGC | AAGTTCACCT CGGCAATGTA |
| AA827835 | CTGGTGCTCA | TTGCGGTGGC | CCGAAACAGC | AAGTTCACCT CGGCAATGTA |
| | 251 | | | 300 |
| AA834537 | CCTGTTTCTG | GGCAACCTGG | CCGCTCCGA | TCTACTGGCA GGCCTGGCCT |
| AA804628 | CCTGTTTCTG | GGCAACCTGG | CCGCTCCGA | TCTACTGGCA GGCCTGGCCT |
| AA827835 | CCTGTTTCTG | GGCAACCTGG | CCGCTCCGA | TCTACTGGCA GGCCTGG. CT |
| | 301 | | | 350 |
| AA834537 | TCGTAGCCAA | TACCTTGCTC | TCTGGCTCTG | TCACGCTGAG GCTGACGCCT |
| AA804628 | TCGTAGCCAA | TACCTTGCTC | TCTGGCTCTG | TCACGCTGAG GCTGACGCCT |
| AA827835 | TCGTAGCCAA | TACCTTGCTC | TCTGGCTCTG | TCACGCTGAG GCTGACGCCT |
| | 351 | | | 400 |
| AA834537 | GTGCAGTGGT | TTGCCCAGGA | CGGTCTGCCT | TCATCAGCCT CTGGGCCTCT |
| AA804628 | GTGCAGTGGT | TTGCCCAGGA | C----- | ----- |
| AA827835 | GTGCAGTGGT | TTGCCCAGGA | ----- | ----- |
| | 401 | | | 450 |
| AA834537 | GTCTTCAGCC | TCCTGGCCAT | CGCCATTGAG | CGCCACGTGG CCATTGCAAA |
| AA804628 | ----- | ----- | ----- | ----- |
| AA827835 | ----- | ----- | ----- | ----- |
| | 451 | | | |
| AA834537 | GG | | | |
| AA804628 | -- | | | |
| AA827835 | -- | | | |

10084507.022602

FIGURE 15 A

1 AAAGCCCCATGGCCCCAGCAGGCCTCTGAGCCCCACCATGGGCAGCTTGTACTCGGAGTA 60
 TTTCCGGGGTACCGGGGTCGTCCGGAGACTCGGGGTGGTACCCGTCCGAACATGAGCCTCAT
 L N P N K V Q E E Y N Y T K E T L E T Q
 61 CCTGAACCCCAACAGGTCCAGGAACACTATAATTATACCAAGGAGACGCTGGAAACGCA 120
 GGAATTGGGGTTGTTCCAGGTCCTTGTGATATTAATATGGTTCTCTCGGACCTTTGCGT
 E T T S R Q V A S A F I V I L C C A I V
 121 GGAGACGACCTCCCGCCAGGTGGCCTCGGGCTTCATCGTTCATCCTCTGTTGCGCCATTGT 180
 CCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAGCAGTAGGAGACAACGCGGTAACA
 V E N L L V L I A V A R N S K F E S A M
 181 GGTGGAACACCTTCTGGTGTCTCATTCGCGTGGCCGAAACAGCAAGTTCACCTCGGCAAT 240
 CCACCTTTTGAAGACCACGAGTAACGCCACCGGGCTTTGTCTTCAAGGTGAGCCGTTA
 Y L F L G N L A A S D L L A G V A F V A
 241 GTACCTGTCTTCTGGGCAACCTGGCCGCTCCGATCTACTGGCAGGCGGTGGCCTTCTGTAGC 300
 CATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGATGACCGTCCGACCGGAAGCATCG
 N T L L S G S V T L R L T P V Q W F A R
 301 CAATACCTTGTCTCTGGCTCTGTCTCAGGCTGAGGCTGACCGCTGTGCACTGTTTGGCCG 360
 GTTATGGAACGAGAGACCGAGACAGTGGACTCCGACTGCGGACACGTCAACAAACGGGC
 E G S A F I T L S A S V F S L L A I A I
 361 GGAGGGCTCTGCTTCATCAGCTCTCGGCTCTGTCTCAGCCTCTGCGCCATCGCCAT 420
 CCTCCCGAGACGGAAGTAGTGCGAGAGCCGAGACAGAAGTCCGAGGACCCGTAGCGGTA
 E R H V A I A K V K L Y G S D K S C R M
 421 TGAGCGCCACGTGGCCATTGCGAAGGTCAAGCTGTATGGCAGCGACAAGAGCTGCCGCAT 480
 ACTCGCGGTGCACCGGTAACGTTCCAGTTCGACATACCGTCTGTCTCTGACGGCGTA
 L L L I G A S W L I S L V L G G L F I L
 481 GCTTCTGCTCATCGGGGCTCGTGGCTCATCTCGCTGCTCTCGGTGGCCTGCCCATCCT 540
 CGAAGACGAGTAGCCCCGGAGCACCGAGTAGAGCGACAGGAGCCACCGACGGGTAGGA
 G W N C L G H L E A C S T V L P L Y A K
 541 TGGCTGGAACTGCTGGGCCACCTCGAGGCTGCTCCACTGTCTGCTCTCTACGCCAA 600
 ACCGACCTTGACGACCCCGGTGGAGCTCCGACGAGGTGACAGGACGGAGAGATGCGGTT
 H Y V L C V V T I F S I I L L A I V A L
 601 GCATTATGTGCTGTGCGTGGTGACCATCTCTCCATCATCCTGTTGGCCATCGTGGCCCT 660
 CGTAATACACGACACGCCACCACTGGTAGAGAGGTAGTAGGACAACCGGTAGCACCGGGA

10084507 022862

| | | |
|------|--|------|
| | Y V R I Y C V V R S S H A D M A A P Q T | |
| 561 | GTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCACGGTGACATGGCCGCCCGCCGAC | 720 |
| | CATGCACGCGTAGATGACGCACCAGGCGAGTTTCGGTCCGACTGTACCGGGCGGGCGTCTG | |
| 721 | L A L L K T V T I V L G V F I V C W L P | 780 |
| | GCTAGCCCTGCTCAAGACGGTCACCATCGTCTAGGCGTCTTTATCGTCTGCTGGCTGCC | |
| | CGATCGGGGACGAGTTCTGCCAGTGGTAGCAGGATCCGCAGAAATAGCAGACGACCGACGG | |
| 781 | A F S I L L L D Y A C P V H S C P I L Y | 840 |
| | CGCCTTCAGCATCGTCCTTCTGGACTATGCCGTGCTCCCGTCCACTCCTGCCCGATCCTCTA | |
| | GCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGGCAGGTGAGCAGCGGCTAGGAGAT | |
| 841 | K A H Y (X) F A V S T L N S L L N P V I Y | 900 |
| | CAAAGCCCACTACTTTTTTCGCCGTCTCCACCGCTGAATTCCTGCTCAACCCCGTCACTTA | |
| | GTTTCGGGTGATGRAAAAGCGGCAGAGGTGGGACTTAAGGGACGAGTTGGGGCAGTAGAT | |
| 901 | T W R S R D L R R E V L R P L Q C W R P | 960 |
| | CACGTGGCGCAGCCGGGACCTGCGCGCGGAGGTGCTTCGGCCGCTGCAGTGCTGGCGGCC | |
| | GTGCACCGCGTCGGCCCTGGACGCGCGCCCTCCACGAAGCCGGCGACGTNACGACCGCCGG | |
| 961 | G V G V Q G R R R G G T F G H H L L P L | 1020 |
| | GGGGGTGGGGGTCAAGGACCGAGGCGGGGCGGGACCCGGGGCCACCACCTCCTGCCACT | |
| | CCCCACCCCCACGTTCTGCTCCGCCCGCCCTGGGGCCCGGTGGTGGAGGACGGTGA | |
| 1021 | R S S S S L E R G M H M P T S P T F L E | 1080 |
| | CCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATGCCACGTCAACCGACGTTTCTGGA | |
| | GCGCTCGAGGTCGAGGGACCTCTCCCCGTACGTGTACGGGTGCAGTGGGTGAAAAGACCT | |
| 1081 | G N T V V * | 1140 |
| | GGGCAACACGGTGGTCTGAGGGTGGGGGTGGACCAACACCAGGCCAGGGCATAGGGGTT | |
| | CCCGTTGTGCCACGAGACTCCACCCCCACCTGGTTGTTGGTCCGGTCCCGTATCCCCAA | |
| 1141 | CATGGAAAGGCCACTGGGTGACCCCAAATA | 1170 |
| | GTACCTTTCCGGTGACCCACTGGGGTTTAT | |

Figure 15B

cDNA sequence of clone pC3-hedg4#36 encoding functional HEDG4 receptor protein.

10084507.022302

ATGGGCAGCTTGTACTCGGAGTACCTGAACCCCAACAAGGTCCAGGAACACTATAATTAT
-----+-----+-----+-----+-----+-----+ 60
TACCCGTCGAACATGAGCCTCATGGACTTGGGGTTGTTCCAGGTCCTTGTGATATTAATA
ACCAAGGAGACGCTGGAAACGCAGGAGACGACCTCCCGCCAGGTGGCCTCGGCCTTCATC
61 -----+-----+-----+-----+-----+ 120
TGGTTCCTCTGCGACCTTTGCGTCTCTGCTGGAGGGCGGTCCACCGGAGCCGGAAGTAG
GTCATCCTCTGTTGCGCCATTGTGGTGGAAAACCTTCTGGTGCTCATTGCGGTGGCCCCGA
121 -----+-----+-----+-----+-----+ 180
CAGTAGGAGACAACCGGTAACACCACCTTTTGAAGACCACGAGTAACGCCACCGGGCT
AACAGCAAGTTCCACTCGGCAATGTACCTGTTTCTGGGCAACCTGGCCGCCTCCGATCTA
181 -----+-----+-----+-----+-----+ 240
TTGTCGTTCAAGGTGAGCCGTTACATGGACAAAGACCCGTTGGACCGGCGGAGGCTAGAT
CTGGCAGGCGTGGCCTTCGTAGCCAATACCTTGCTCTCTGGCTCTGTCACGCTGAGGCTG
241 -----+-----+-----+-----+-----+ 300
GACCGTCCGCACCGGAAGCATCGGTTATGGAACGAGAGACCGAGACAGTGCGACTCCGAC
ACGCCTGTGCAGTGGTTTGGCCGGGAGGGCTCTGCCTTCATCACGCTCTCGGCCTCTGTC
301 -----+-----+-----+-----+-----+ 360
TGCGGACACGTCACCAAACGGGCCCTCCCGAGACGGAAGTAGTGCAGAGACCGGAGACAG
TTCAGCCTCCTGGCCATCGCCATTGAGCGCCACGTGGCCATTGCCAAGGTCAAGCTGTAT
361 -----+-----+-----+-----+-----+ 420
AAGTCGGAGGACCGGTAGCGTAACTCGCGGTGCACCGGTAACGGTTCCAGTTCGACATA
GGCAGCGACAAGAGCTGCCGCATGCTTCTGCTCATCGGGGCCTCGTGGCTCATCTCGCTG
421 -----+-----+-----+-----+-----+ 480
CCGTCGCTGTTCTCGACGGCGTACGAAGACGAGTAGCCCCGAGCACCGAGTAGAGCGAC
GTCTCTCGGTGGCCTGCCCATCCTTGGCTGGAACTGCCTGGGGCCACCTCGAGGCCTGCTCC
481 -----+-----+-----+-----+-----+ 540
CAGGAGCCACCGGACGGGTAGGAACCGACCTTGACGGACCCGGTGGAGCTCCGGACGAGG
ACTGTCCTGCCTCTCTACGCCAAGCATTATGTGCTGTGCGTGGTGACCATCTTCTCCATC
541 -----+-----+-----+-----+-----+ 600
TGACAGGACCGGAGAGATGCGGTTGTAATACACGACACGCACCACTGGTAGAAGAGGTAG
ATCCTGTTGGCCGTCGTGGCCCTGTACGTGCGCATCTACTGCGTGGTCCGCTCAAGCCAC
601 -----+-----+-----+-----+-----+ 660
TAGGACAACCGGCAGCACCGGGACATGCACGCTAGATGACGCACCAGGCGAGTTCGGTG
GCTGACATGGCCGCCCCGAGACGCTAGCCCTGCTCAAGACGGTCACCATCGTGCTAGGC
661 -----+-----+-----+-----+-----+ 720
CGACTGTACCGGCGGGGCGTCTGCGATCGGGACGAGTTCTGCCAGTGGTAGCACGATCCG
GTCTTTATCGTCTGCTGGCTGCCCCGCTTCAGCATCCTCCTTCTGGACTATGCCTGTCCC
721 -----+-----+-----+-----+-----+ 780

20081107 10:23:02

CAGAAATAGCAGACGACCGACGGGCGGAAGTCGTAGGAGGAAGACCTGATACGGACAGGG
GTCCACTCCTGCCCCGATCCTCTACAAAGCCCACCTACCTTTTCGCCGTCTCCACCCTGAAT 781 840
-----+-----+-----+-----+-----+-----+
CAGGTGAGGACGGGCTAGGAGATGTTTCGGGTGATGGAAAAGCGGCAGAGGTGGGACTTA
TCCCTGCTCAACCCCGTCATCTACACGTGGCGCAGCCGGGACCTGCGGCGGGAGGTGCTT 841 900
-----+-----+-----+-----+-----+-----+
AGGGACGAGTTGGGGCAGTAGATGTGCACCGCGTCGGCCCTGGACGCCGCCCTCCACGAA
CGGCCGCTGCAGTGCTGGCGGCCGGGGGTGGGGGTGCAAGGACGGAGGCGGGGCGGGACC 901 960
-----+-----+-----+-----+-----+-----+
GCCGGCGACGTCACGACCGCGGCCCGCCCCACCCCCACGTTCTGCTCCGCCCCGCCCTGG
CCGGGCCACCACTCCTGCCACTCCGCAGCTCCAGCTCCCTGGAGAGGGGCATGCACATG 961 1020
-----+-----+-----+-----+-----+-----+
GGCCCGGTGGTGGAGGACGGTGAGGCGTCGAGGTCGAGGGACCTCTCCCCGTACGTGTAC
CCCACGTCACCCACGTTTCTGGAGGGCAACACGGTGGTCTGA 1021 1062
-----+-----+-----+-----+-----+-----+
GGGTGCAGTGGGTGCAAAGACCTCCCGTTGTGCCACCAGACT

FIGURE 16 A

1 MGSLYSEYLN PNKVOEHYNY TKETLETOET TSQVASAFI VILCCAIVVE
 51 NLLVLIARVAR NSKPHSAMYL FLGNLAASDL LAGVAFVANT LLSGGSVTLRL
 101 TFWQWFAREG SAFITLSAEV FSLIAIAIER HVAIAKVLY GSDKSCRMIL
 151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLGCVVTIESI
 201 ILLAIVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTVILG VFIVCWLPAP
 251 SILLLDYACP VHSCPILYKA HYKEAVSTLN SLLAPVIYTW RSRDLRREVL
 301 RFLQCWRPGV GVQGRRRGGT PGHLLPLRS SSSLERGMMH PTSFTFLEGN
 351 TVV*

Conserved features of G-protein coupled receptors include:

| | |
|----------------------------------|--------------------|
| N-terminal extracellular domain: | Residues 1 - 36 |
| TM-I: | Residues 37 - 57 |
| Intracellular loop 1: | Residues 58 - 68 |
| TM-II: | Residues 69 - 92 |
| Extracellular loop 1: | Residues 93 - 111 |
| TM-III: | Residues 112 - 130 |
| Intracellular loop 2: | Residues 131 - 149 |
| TM-IV: | Residues 150 - 168 |
| Extracellular loop 2: | Residues 169 - 185 |
| TM-V: | Residues 186 - 210 |
| Intracellular loop 3: | Residues 211 - 232 |
| TM-VI: | Residues 233 - 254 |
| Extracellular loop 3: | Residues 255 - 266 |
| TM-VII: | Residues 267 - 285 |
| C-terminal cytoplasmic domain: | Residues 286 - 353 |

Potential post-transcriptional modification sites:

| | |
|------------------|---------------------------------------|
| N-glycosylation: | Residues 19 |
| Phosphorylation: | Residues 142, 145, 219, 289, 332, 345 |
| Myristylation: | Residues 141, 318 |

20250707 10:54:00

Figure 16B

Predicted amino acid sequence of HEDG4 polypeptide encoded by pC3-hedg4#36.

1 MGSLYSEYLN PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE
51 NLLVLIAVAR NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRRL
101 TPVQWFAREG SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL
151 LIGASWLISL VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI
201 ILLAVVALYV RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAF
251 SILLLDYACP VHSCPILYKA HYLFAVSTLN SLLNPVIYTW RSRDLRREVL
301 RPLQCWRPGV GVQGRRRGGT PGHHLLPLRS SSSLERGMHM PTSPTFLEGN
351 TVV

10084507.DP2E02

Figure 17B

Alignment of HEDG4 with pC3-hedg4#36 translation product and rat H218 (REDG4). Differences between pC3-hedg4#36 translation product and previously determined HEDG4 polypeptide are indicated in reverse text. Differences between rat and human edg-4 polypeptide sequences are shown in bold, shaded text.

| | | | |
|----------|----------|---------|--|
| | 1 | | 50 |
| HEDG4 | MGS | LYSEYLN | PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE |
| HEDG4#36 | MGS | LYSEYLN | PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE |
| REDG4 | MGS | LYSEYLN | PNKVQEHYNY TKETLETQET TSRQVASAFI VILCCAIVVE |
| | 51 | | 100 |
| HEDG4 | NLLVLI | AVAR | NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL |
| HEDG4#36 | NLLVLI | AVAR | NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL |
| REDG4 | NLLVLI | AVAR | NSKFHSAMYL FLGNLAASDL LAGVAFVANT LLSGSVTLRL |
| | 101 | | 150 |
| HEDG4 | TPVQWF | AREG | SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL |
| HEDG4#36 | TPVQWF | AREG | SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL |
| REDG4 | TPVQWF | AREG | SAFITLSASV FSLLAIAIER HVAIAKVKLY GSDKSCRMLL |
| | 151 | | 200 |
| HEDG4 | LIGASWL | LISL | VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI |
| HEDG4#36 | LIGASWL | LISL | VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI |
| REDG4 | LIGASWL | LISL | VLGGLPILGW NCLGHLEACS TVLPLYAKHY VLCVVTIFSI |
| | 201 | | 250 |
| HEDG4 | ILLAVVAL | YV | RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP |
| HEDG4#36 | ILLAVVAL | YV | RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP |
| REDG4 | ILLAVVAL | YV | RIYCVVRSSH ADMAAPQTLA LLKTVTIVLG VFIVCWLPAP |
| | 251 | | 300 |
| HEDG4 | SILLLDY | ACP | VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL |
| HEDG4#36 | SILLLDY | ACP | VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL |
| REDG4 | SILLLDY | ACP | VHSCPILYKA HYXFAVSTLN SLLNPVIYTW RSRDLRREVL |
| | 301 | | 350 |
| HEDG4 | RPLQCWR | PGV | GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN |
| HEDG4#36 | RPLQCWR | PGV | GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN |
| REDG4 | RPLQCWR | PGV | GVQGRRRGGT PGHLLPLRS SSSLERGMHM PTSPTFLEGN |
| | 351 | | |
| HEDG4 | TVV~ | | |
| HEDG4#36 | TVV~ | | |
| REDG4 | TVV~ | | |

10084507.022802

Figure 18A.

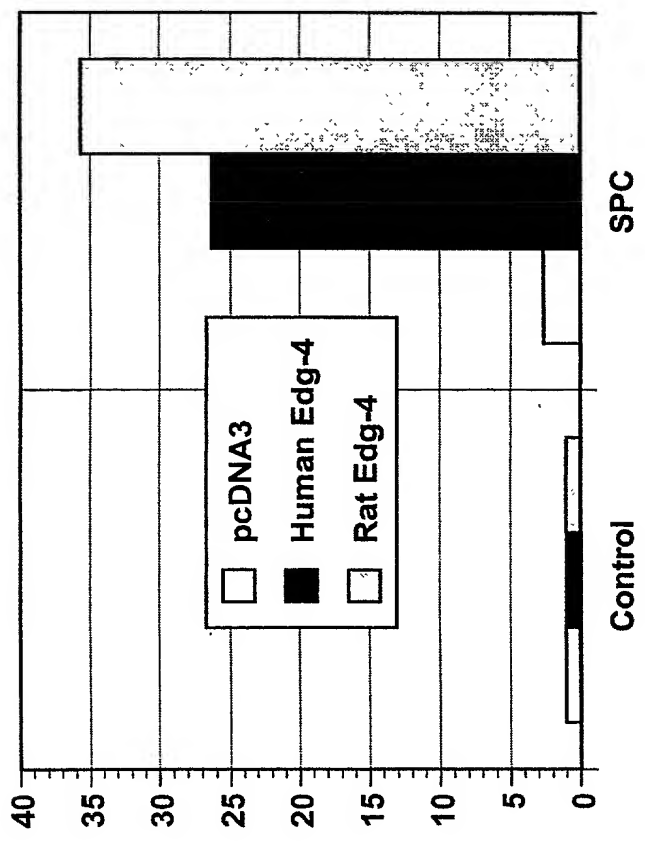


Figure 18B.

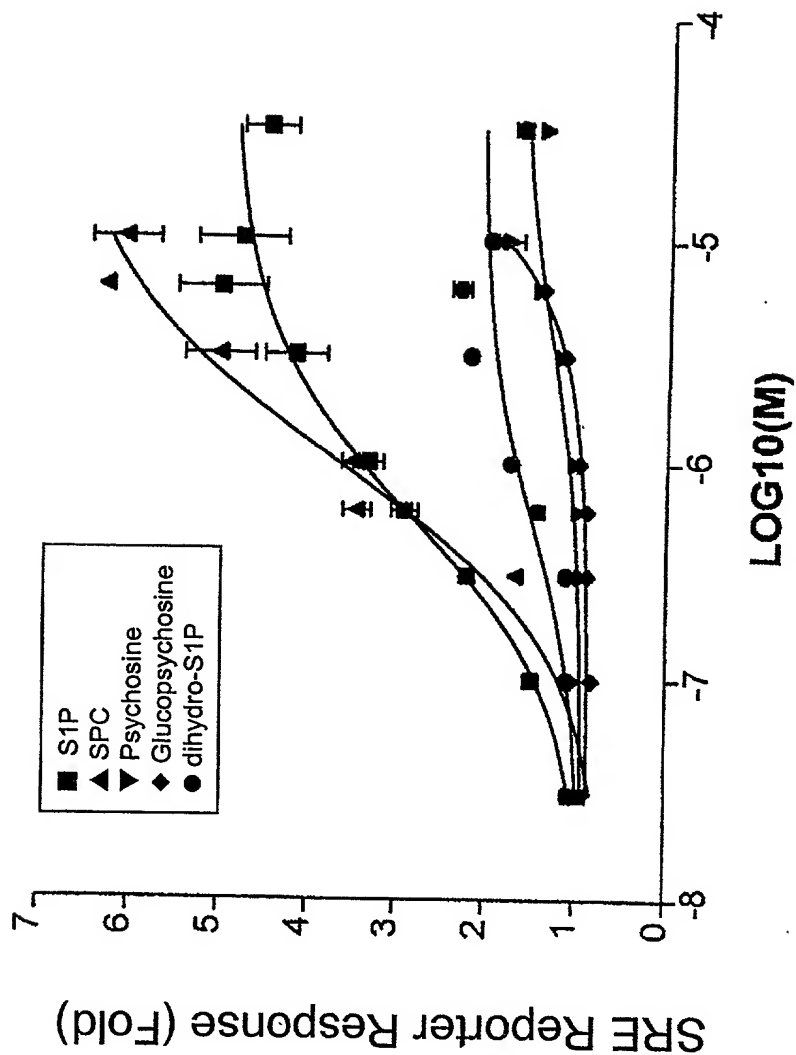


Figure 19.

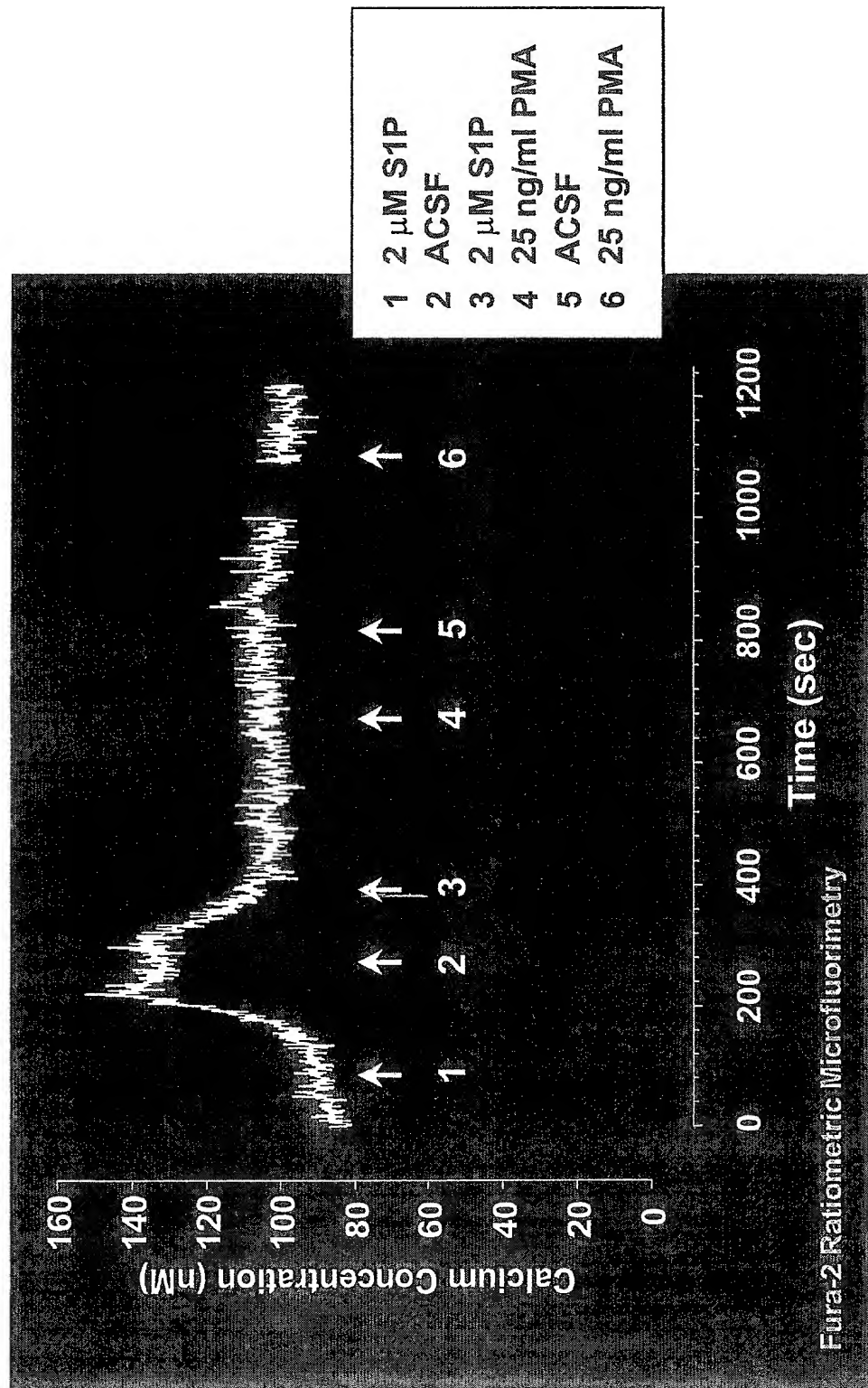


Figure 20.

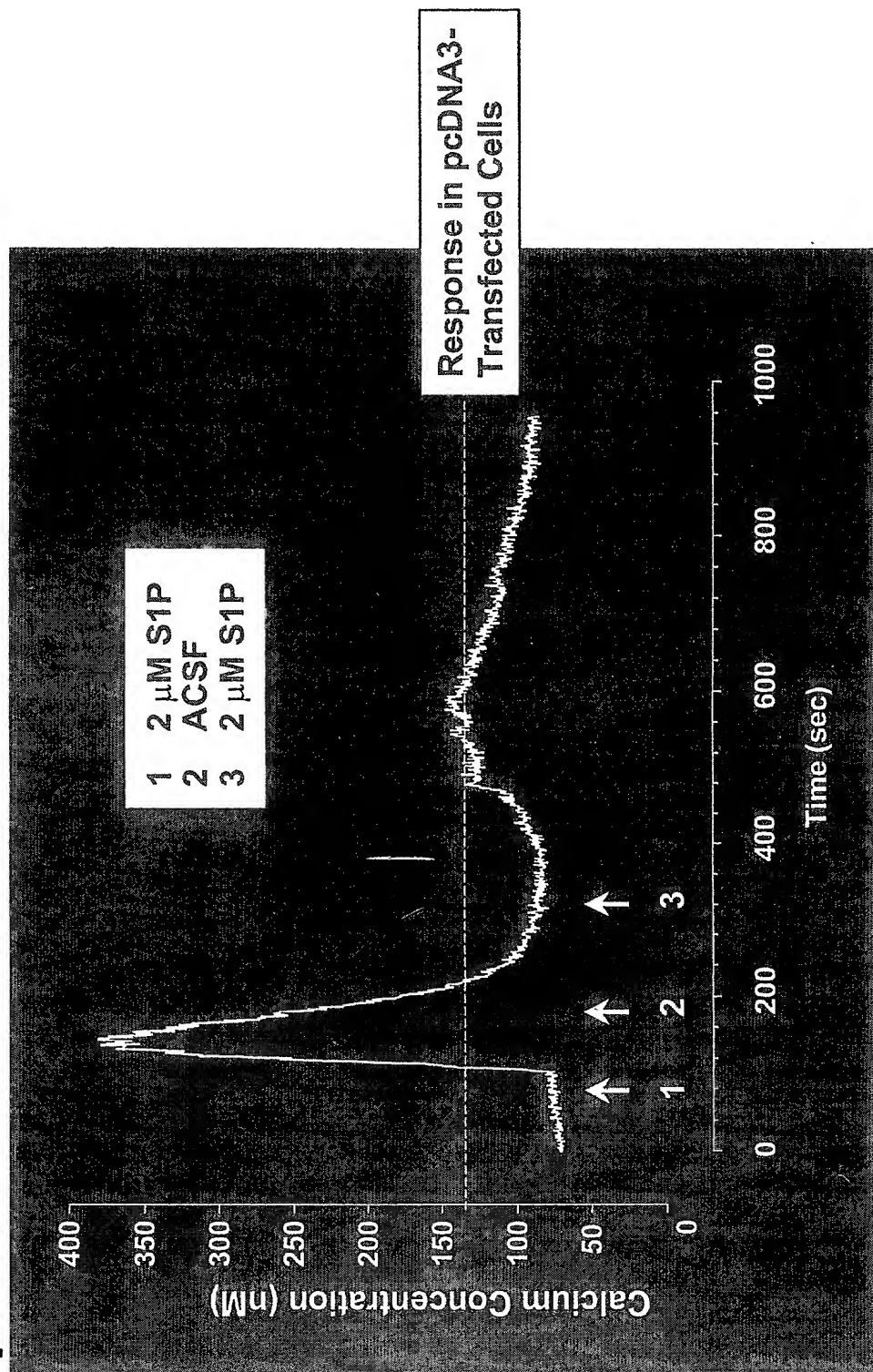


Figure 21. Human Edg-6 Amino Acid Sequence.

1 MVIMGQCYINETIGFFYNNSGKELSSHWRPKDVVVALGLTVSVLVLLTNLLVIAAIASN 60
-----+-----+-----+-----+-----+-----+
61 RRFHQPIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLDTSLTASVA 120
-----+-----+-----+-----+-----+-----+
121 TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALGLGLLPAHSWHCLCALDRCSR 180
-----+-----+-----+-----+-----+-----+
181 MAPLLSRSYLAVWALSSLLVFLLMVAVYTRIFFYVRRRVQRM AEHVSCHPRYRETTLSLV 240
-----+-----+-----+-----+-----+-----+
241 KTVVILGAFVVCWTPGQVVL LLDGLGCESC NVLAVEKYFLL LAEANS LVNAAVYSCRDA 300
-----+-----+-----+-----+-----+-----+
301 EMRRTFRRLCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMDSTL* 352
-----+-----+-----+-----+-----+-----+-----

208220 2084800

Figure 22. Human Edg-6 Sequence

1 ATGGTCATCATGGGCCAGTGCTACTACAACGAGACCATCGGCTTCTTCTATAACAACAGT 60
 -----+-----+-----+-----+-----+-----+
 TACCAGTAGTACCCGGTCACGATGATGTTGCTCTGGTAGCCGAAGAAGATATTGTTGTCA
 61 GGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGGTCGTGGTGGCACTGGGGCTG 120
 -----+-----+-----+-----+-----+-----+
 CCGTTTCTCGAGTCGAGGGTGACCGCCGGGTTCTACACCAGCACCACCGTGACCCCGAC
 121 ACCGTCAGCGTGCTGGTGCTGCTGACCAATCTGCTGGTCATAGCAGCCATCGCCTCCAAC 180
 -----+-----+-----+-----+-----+-----+
 TGGCAGTCGCACGACCAGCAGACTGGTTAGACGACCAGTATCGTCGGTAGCGGAGGTTG
 181 CGCCGCTTCCACCAGCCCATCTACTACCTGCTCGGCAATCTGGCCGCGGCTGACCTCTTC 240
 -----+-----+-----+-----+-----+-----+
 GCGGCGAAGGTGGTCGGGTAGATGATGGACGAGCCGTTAGACCGGCGCCGACTGGAGAAG
 241 GCGGGCGTGGCC'TACCTCTTCCTCATGTTCCACACTGGTCCCCGCACAGCCCGACTTTCA 300
 -----+-----+-----+-----+-----+-----+
 CGCCCGCACC GGATGGAGAAGGAGTACAAGGTGTGACCAGGGGCGTGTCGGGCTGAAAGT
 301 CTTGAGGGGCTGGTTCCTGCGGCAGGGCTTGCTGGACACAAGCCTCACTGCGTCGGTGGCC 360
 -----+-----+-----+-----+-----+-----+
 GAACTCCCGACCAAGGACGCCGTCCCGAACGACCTGTGTTGAGAGTGACGCAGCCACCGG
 361 ACACTGCTGGCCATCGCCGTGGAGCGGCACCGCAGTGTGATGGCCGTGCAGCTGCACAGC 420
 -----+-----+-----+-----+-----+-----+
 TGTGACGACCGGTAGCGGCACCTCGCCGTGGCGTCACACTACCGGCACGTGACGTGTGCG
 421 CGCCTGCCCCGTGGCCGCGTGGTCATGCTCATTGTGGGCGTGTTGGGTGGCTGCCCTGGGC 480
 -----+-----+-----+-----+-----+-----+
 GCGGACGGGGCACCGGCGCACCAGTACGAGTAACACCCGCACACCCACCGACGGGACCCG
 481 CTGGGGCTGCTGCCTGCCACTCCTGGCACTGCCTCTGTGCCCTGGACCGCTGCTCACGC 540
 -----+-----+-----+-----+-----+-----+
 GACCCCGACGACGGACGGGTGAGGACCGTGACGGAGACACGGGACCTGGCGACGAGTGCG
 541 ATGGCACCCCTGCTCAGCCGCTCCTATTTGGCCGTCTGGGCTCTGTGAGCCTGCTTGTC 600
 -----+-----+-----+-----+-----+-----+
 TACCGTGGGGACGAGTCGCGGAGGATAAACCGGCAGACCCGAGACAGCTCGGACGAACAG
 601 TTCCTGCTCATGGTGGCTGTGTACACCCGCATTTCTTCTACGTGCGGCGGCGAGTGCAG 660
 -----+-----+-----+-----+-----+-----+
 AAGGACGAGTACCACCGACACATGTGGGCGTAAAGAAGATGCACGCCGCCGCTCACGTC
 661 CGCATGGCAGAGCATGTCAGCTGCCACCCCGCTACCGAGAGACCACGCTCAGCCTGGTC 720
 -----+-----+-----+-----+-----+-----+
 GCGTACCGTCTCGTACAGTCGACCGTGGGGGCGATGGCTCTCTGCTGCGAGTCGGACCAG
 721 AAGACTGTTGTATCATCCTGGGGGCGTTCTGTTGCTGCTGGACACCAGGCCAGGTGGTA 780
 -----+-----+-----+-----+-----+-----+
 TTCTGACAACAGTAGTAGGACCCCGCAAGCACCAGACGACCTGTGGTCCGGTCCACCAT
 781 CTGCTCCTGGATGGTTTAGGCTGTGAGTCCTGCAATGTCCTGGCTGTAGAAAAGTACTTC 840
 -----+-----+-----+-----+-----+-----+
 GACGAGGACCTACCAAATCCGACACTCAGGACGTTACAGGACCGACATCTTTTCATGAAG

20220720 1004507 022800

841 CTACTGcTGGCCGAGGCCAACTCACTGGTCAATGCTGCTGTGTACTCTTGCCGAGATGCT
 -----+-----+-----+-----+-----+-----+ 900
 GATGACgACCGGCTCCGGTTGAGTGACCAGTTACGACGACACATGAGAACGGCTCTACGA

 901 GAGATGCGCCGCACCTTCCGCGCCTTCTCTGCTGCGCGTGCCTCCGCCAGTCCACCCGC
 -----+-----+-----+-----+-----+-----+ 960
 CTCTACGCGGCGTGGAAGGCGGCGGAAGAGACGACGCGCACGGAGGCGGTCAGGTGGGCG

 961 GAGTCTGTCCACTATACATCCTCTGCCCAGGGAGGTGCCAGCACTCGCATCATGCTTCCC
 -----+-----+-----+-----+-----+-----+ 1020
 CTCAGACAGGTGATATGTAGGAGACGGGTCCCTCCACGGTCGTGAGCGTAGTACGAAGGG

 1021 GAGAACGGCCACCCACTGATGGACTCCACCCTTTAG
 -----+-----+-----+-----+-----+ 1056
 CTCTTGCCGGTGGGTGACTACCTGAGGTGGGAAATC

202207054800T

Figure 23.

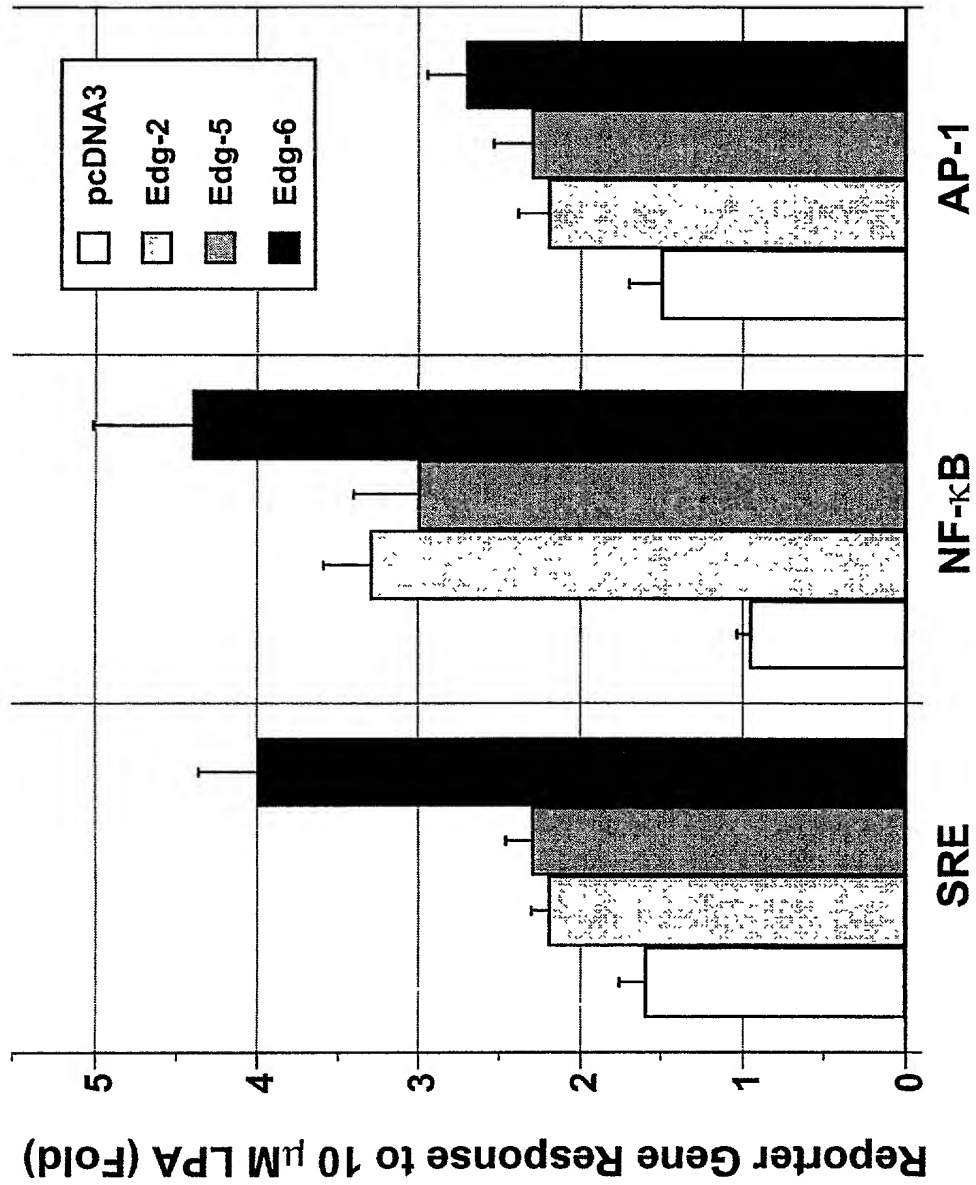


Figure 24.

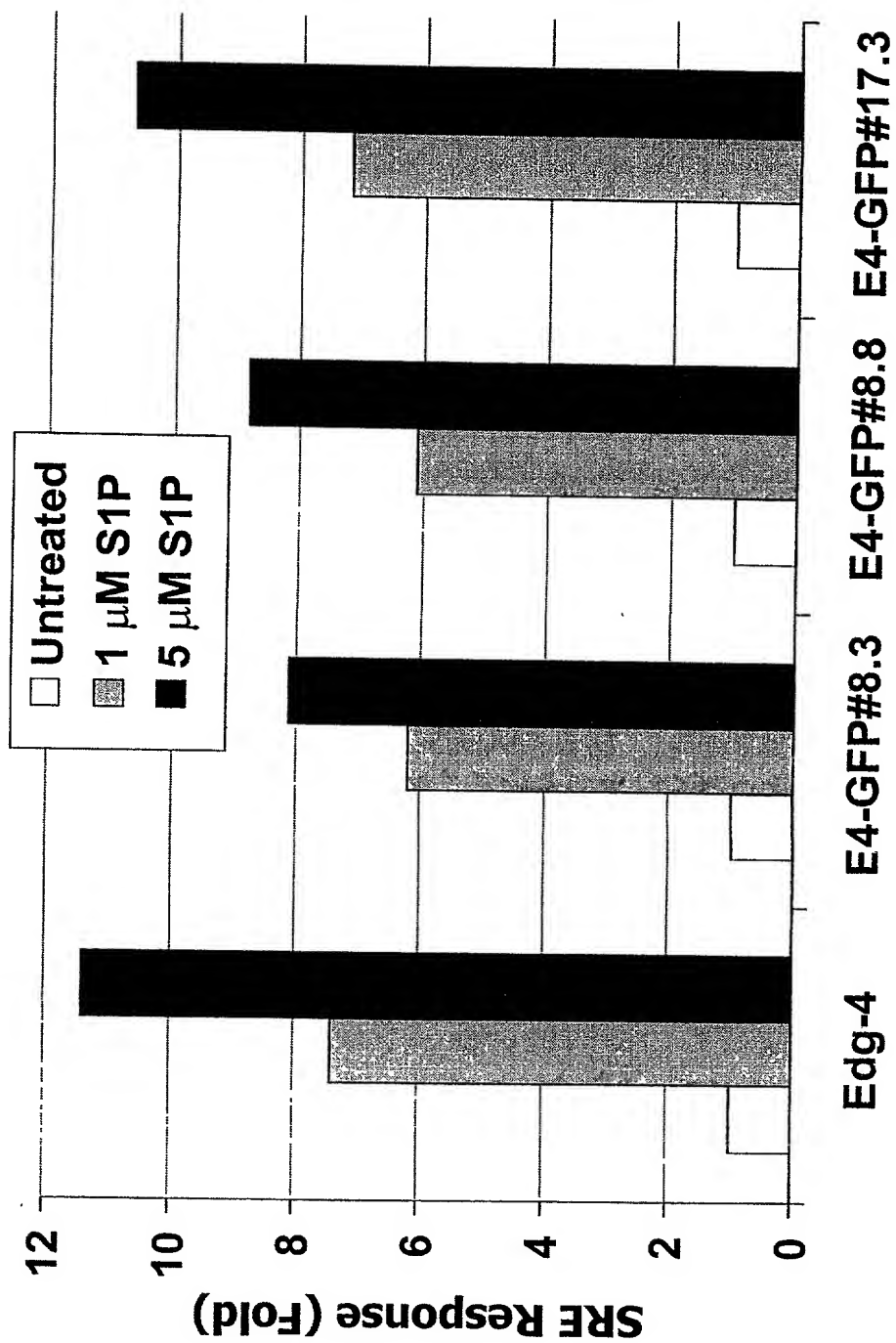
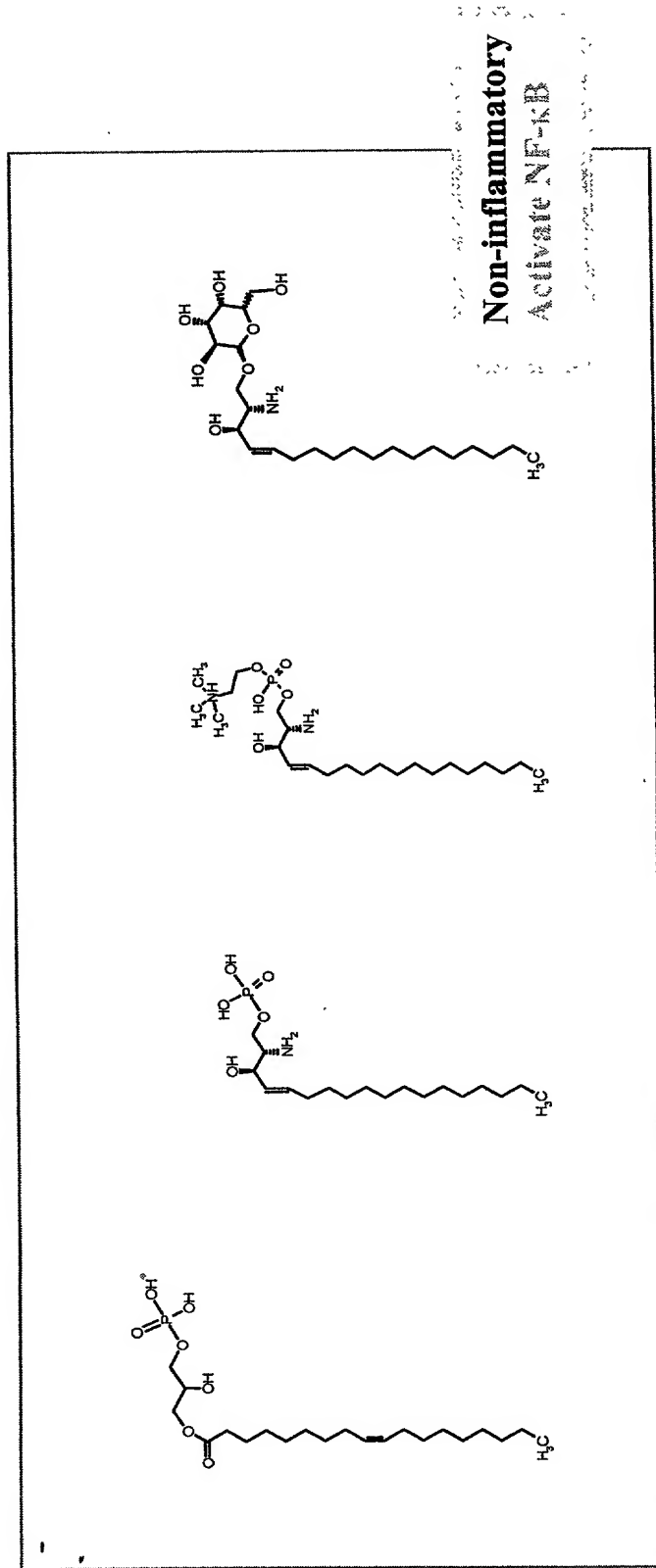


Figure 25.



Psychoseine

Edg-3
Edg-4

SPC

Edg-1
Edg-3
Edg-4
Edg-7

S1P

Edg-1
Edg-3
Edg-4
Edg-7

LPA

Edg-2
Edg-5
Edg-6